

# SCORE Search Results Details for Application 10591347 and Search Result 20110118\_143645\_seq2sub1636a.rng.

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This page gives you Search Results detail for the Application 10591347 and Search Result 20110118\_143645\_seq2sub1636a.rng.

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GenCore version 6.3

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2011, 23:09:15 ; Search time 1294 Seconds  
(without alignments)  
56139.102 Million cell updates/sec

Title: SEQ2SUB1636A  
Perfect score: 3424  
Sequence: 1 aggatcagaacaatgcctcc.....taaactagttcatttcaaaa 3424

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18225500 seqs, 10608060480 residues

Total number of hits satisfying chosen parameters: 36451000

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_201023:\*  
1: geneseqn1:\*  
2: geneseqn2:\*  
3: geneseqn3:\*  
4: geneseqn4:\*  
5: geneseqn5:\*  
6: geneseqn6:\*  
7: geneseqn7:\*  
8: geneseqn8:\*

9: geneseqn9:\*

## SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	3422.4	99.9	3424	1	AAS14365	Aas14365 cDNA enco
2	3422.4	99.9	3424	1	ABL59523	Abl59523 Human pho
3	3422.4	99.9	3424	2	ADE85076	Ade85076 Farnesyl
4	3422.4	99.9	3424	4	ADZ00490	Adz00490 p110-beta
5	3422.4	99.9	3424	4	AEH10445	Aeh10445 PIK3CA cD
6	3422.4	99.9	3424	4	AED31618	Aed31618 cDNA (SEQ
7	3422.4	99.9	3424	4	AEG93388	Aeg93388 Human tum
8	3410.4	99.6	3412	1	AAQ51156	Aaq51156 Human p11
9	3410.4	99.6	3412	4	AED31617	Aed31617 cDNA (SEQ
10	3410.4	99.6	3423	3	ADU05935	Adu05935 Novel bro
11	3338	97.5	3426	6	ARC02473	Arc02473 DNA fragm
12	3338	97.5	3724	4	AEK54940	Aek54940 Human PIK
13	3338	97.5	3724	5	AER29796	Aer29796 Breast ca
14	3338	97.5	3724	7	ARV60468	Arv60468 Human PIK
15	3338	97.5	3724	7	ARW65283	Arw65283 Human PIK
16	3338	97.5	3724	7	ATM52123	Atm52123 Human PIK
17	3338	97.5	3724	7	ATS16021	Ats16021 Human pho
18	3338	97.5	3724	8	AWY98731	Awy98731 Human PIK
19	3338	97.5	3724	8	AWY98891	Awy98891 Human PIK
20	3338	97.5	3724	8	AWY98894	Awy98894 Human PIK
21	3338	97.5	3724	9	AXU25358	Axu25358 Human pho
22	3338	97.5	3724	9	AYE41305	Aye41305 Human PIK
23	3279.4	95.8	4326	8	AWY98838	Awy98838 Human PIK
24	3205.4	93.6	3207	2	ADH68168	Adh68168 DNA encod
25	3205.4	93.6	3207	4	AEF64785	Aef64785 Human pho
26	3145	91.9	7923	8	AWO77361	Awo77361 Expressio
27	3144.6	91.8	3207	4	AEK13514	Aek13514 Phosphati
28	3144.6	91.8	3207	7	ARL60529	Arl60529 Human pho
29	3143	91.8	3207	4	AEK13519	Aek13519 Phosphati
30	3141.4	91.7	3207	4	AEK13515	Aek13515 Phosphati
31	3137	91.6	3498	1	AAQ57012	Aaq57012 PtdIns 3-
32	3118.8	91.1	3210	4	AEK13511	Aek13511 Phosphati
33	3007	87.8	3207	1	AAQ51155	Aaq51155 p110 cDNA
34	2640.6	77.1	3207	8	AWY98836	Awy98836 Human PIK
35	2640.6	77.1	3207	8	AWY98892	Awy98892 Human PIK
36	1687.6	49.3	8421	2	ACN43202	Acn43202 Human dia
37	1515.8	44.3	2397	1	AFS82080	Afs82080 Human tra
38	1183.4	34.6	1792	3	ADR39810	Adr39810 Human kin
39	697.4	20.4	2872	8	AWY98893	Awy98893 Human PIK
40	564	16.5	741	1	AAA02190	Aaa02190 Human col
41	564	16.5	741	4	AGD33161	Agd33161 Human pol
42	530	15.5	716	4	AEK18520	Aek18520 Human PIK
43	460.8	13.5	3213	1	AAC65690	Aac65690 Human PI3

44	460.8	13.5	3213	1	AAS14366	Aas14366 cDNA enco
45	460.8	13.5	3213	1	ABV78026	Abv78026 Hypoxia-r

## ALIGNMENTS

## RESULT 1

## AAS14365

ID AAS14365 standard; cDNA; 3424 BP.

XX

AC AAS14365;

XX

DT 11-JUN-2007 (revised)

DT 12-MAR-2002 (first entry)

XX

DE cDNA encoding human p110alpha isoform of PI3-kinase.

XX

KW Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform; LASP-1;

KW cancer; inflammatory disease; ophthalmic disorder; SH3 domain;

KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;

KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13. .3219

FT /\*tag= a

FT /product= "p110alpha isoform of PI3-kinase"

XX

PN WO200185986-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-US015065.

XX

PR 10-MAY-2000; 2000US-0203346P.

XX

PA (ICOS-) ICOS CORP.

XX

PI Sadhu C;

XX

DR WPI; 2002-075252/10.

DR P-PSDB; AAU09687.

DR PC:NCBI; gi472990.

DR PC\_ENCPRO:NCBI; gi472991.

XX

PT Identifying a modulator of p110delta polypeptide binding to SH3 domain-

PT containing polypeptides e.g. LASP-1, comprising allowing the binding

```
Query Match          99.9%;   Score 3422.4;   DB 1;   Length 3424;
Best Local Similarity 99.9%;
Matches 3423;   Conservative    0;   Mismatches    1;   Indels      0;   Gaps      0;
```

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300

Db	241	GCAGAAAGGGAAGAATTTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAATAGTGGTGATTTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAATAGTGGTGATTTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020

Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740

Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAA AATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAA AATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTA ACTTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTA ACTTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTT CATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTT CATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520

Db	2461	 ATTCGTATTATGGAAAATATCTGGCAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	 GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	 ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	 CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	 TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Db	2761	 CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	 TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	 ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941	 TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	 CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	 GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	 GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240



Db	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 2  
ABL59523  
ID ABL59523 standard; cDNA; 3424 BP.  
XX  
AC ABL59523;  
XX  
DT 11-JUN-2007 (revised)  
DT 16-JUL-2002 (first entry)  
XX  
DE Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.  
XX  
KW Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme; tumour;  
KW lipid associated gene; lipid metabolism; lipid synthesis;  
KW chromosome 3q26.3; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200227028-A1.  
XX  
PD 04-APR-2002.  
XX  
PF 27-SEP-2001; 2001WO-US030366.  
XX  
PR 28-SEP-2000; 2000US-00676052.  
XX  
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.  
XX  
PI Skinner MK, Patton JL, Chaudhary J;  
XX  
DR WPI; 2002-405056/43.

DR PC:NCBI; gi472990.  
DR PC\_ENCPRO:NCBI; gi472991.  
XX  
PT Identifying tumor characteristics in a tissue sample taken from a  
PT patient, involves determining the copy number or expression level of  
PT genes associated with lipid metabolism, synthesis or action.  
XX  
PS Example 1; Page 82-83; 113pp; English.  
XX  
CC The present invention describes a method for identifying tumour  
CC characteristics, comprising measuring a copy number or expression level  
CC of at least two genes associated with lipid metabolism, synthesis, or  
CC action in cells from a patient tissue sample, and comparing the results  
CC with a copy number or expression level of the genes in a normal cell.  
CC Also described is an array of nucleic acid polymers immobilised on a  
CC solid support, comprising a solid support, at least two different nucleic  
CC acid polymers which are each specific for a different gene associated  
CC with lipid metabolism, synthesis or action, where each nucleic acid  
CC polymer is located at a predetermined position on the solid support, and  
CC the array comprises nucleic acid polymers which are specific for less  
CC than 100 genes other than the selected genes. The method is useful for  
CC determining tumour characteristics in a tissue sample taken from a  
CC patient. The present sequence represents a human lipid-associated gene  
CC related cDNA sequence, which is used in the exemplification of the  
CC present invention  
CC  
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed  
CC information from BOND.  
XX  
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match		99.9%;	Score 3422.4;	DB 1;	Length 3424;
Best Local Similarity		99.9%;			
Matches 3423;		Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60		
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60		
Qy	61	CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120		
Db	61	CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120		
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180		
Db	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180		
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240		

Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAGTGGTGATTTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAGTGGTGATTTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960

Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680

Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460

Db	2401	 AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	 ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	 GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	 ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	 CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	 TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Db	2761	 CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	 TTTTTGGATCACAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	 ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Db	2941	 TTTGAGAGGTTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	 CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	 GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180

Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 3

ADE85076

ID	ADE85076 standard; DNA; 3424 BP.
XX	
AC	ADE85076;
XX	
DT	11-JUN-2007 (revised)
DT	29-JAN-2004 (first entry)
XX	
DE	Farnesyl transferase inhibitor modulated leukemia associated gene #295.
XX	
KW	ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW	quinolinone; leukemia; cancer.
XX	
OS	Homo sapiens.
XX	
PN	WO2003038129-A2.
XX	
PD	08-MAY-2003.
XX	
PF	30-OCT-2002; 2002WO-US034784.
XX	
PR	30-OCT-2001; 2001US-0338997P.
PR	30-OCT-2001; 2001US-0340081P.
PR	30-OCT-2001; 2001US-0340938P.
PR	30-OCT-2001; 2001US-0341012P.

XX  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
XX  
PI Raponi M;  
XX  
DR WPI; 2003-513497/48.  
DR PC:NCBI; gi472990.  
DR PC\_ENCPRO:NCBI; gi472991.  
XX  
PT Determining whether a patient will respond to treatment with a farnesyl  
PT transferase inhibitor, by analyzing the expression of gene that is  
PT differentially modulated in the presence of the inhibitor.  
XX  
PS Disclosure; SEQ ID NO 295; 346pp; English.  
XX  
CC The invention relates to a method of determining whether a patient will  
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by  
CC analyzing the expression of gene that is differentially modulated in the  
CC presence of an FTI. The method is useful for determining whether a  
CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-  
CC chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-  
CC methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a  
CC patient with leukemia with FTI if the analysis indicates that the patient  
CC will respond. This sequence corresponds to a gene whose expression may be  
CC modulated in the presence of FTI.  
CC  
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed  
CC information from BOND.  
XX  
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 99.9%; Score 3422.4; DB 2; Length 3424;  
Best Local Similarity 99.9%;  
Matches 3423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240



Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAAGTGGTGATTTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAAGTGGTGATTTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960

Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680

Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460

Db	2401	 AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	 ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	 GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	 ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	 CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	 TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Db	2761	 CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	 TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	 ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Db	2941	 TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	 CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	 GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180

Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 4  
ADZ00490  
ID ADZ00490 standard; cDNA; 3424 BP.  
XX  
AC ADZ00490;  
XX  
DT 11-JUN-2007 (revised)  
DT 16-JUN-2005 (first entry)  
XX  
DE p110-beta coding sequence.  
XX  
KW ss; Anorectic; Antidiabetic; p110-beta; phosphoinositide 3-kinase; p85;  
KW ras; insulin resistance; obesity; gene.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 13. .3219  
FT /\*tag= a  
XX  
PN WO2005031341-A2.  
XX  
PD 07-APR-2005.  
XX  
PF 28-SEP-2004; 2004WO-IB003926.  
XX

PR 29-SEP-2003; 2003US-0507226P.  
PR 13-JUL-2004; 2004US-0587333P.  
XX  
PA (PFIZ ) PFIZER HEALTH AB.  
XX  
PI Bougneres P;  
XX  
DR WPI; 2005-273421/28.  
DR P-PSDB; ADZ00491.  
DR GENBANK; Z29090.  
DR PC:NCBI; gi472990.  
DR PC\_ENCPRO:NCBI; gi472991.  
XX  
PT Predicting a subject's likelihood of developing insulin resistance,  
PT useful for treating insulin resistance and obesity, comprises determining  
PT in a subject the identity of an allele at position 100 of a specific  
PT sequence.  
XX  
PS Disclosure; SEQ ID NO 2; 88pp; English.  
XX  
CC This sequence represents the p110-beta gene. p110-beta is a catalytic  
CC subunit of a phosphoinositide 3-kinase, which also comprises a regulatory  
CC subunit of about 85 kD. The p110 protein comprises a kinase domain at the  
CC C-terminus, and a p85 and ras binding domain at the N-terminus. The  
CC method of the invention for predicting a subject's likelihood of  
CC developing insulin resistance comprises determining in a subject the  
CC identity of the nucleotide present at a position corresponding to  
CC position -359 of the p110-beta gene , where the allele comprising the  
CC nucleotide is correlated with an increased or decreased likelihood of  
CC developing insulin resistance. The method of the invention is useful for  
CC treating obesity and insulin resistance and for assessing and conducting  
CC clinical trials of medicaments.  
CC  
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed  
CC information from BOND.  
XX  
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 99.9%; Score 3422.4; DB 4; Length 3424;  
Best Local Similarity 99.9%;  
Matches 3423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120

Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840

Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620



Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340

Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060

Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 5

AEH10445

ID AEH10445 standard; cDNA; 3424 BP.

XX

AC AEH10445;

XX

DT 11-JUN-2007 (revised)

DT 01-JUN-2006 (first entry)

XX

DE PIK3CA cDNA SEQ ID 831.

XX

KW gene expression; prognosis; diagnosis; DNA microarray;

KW colorectal disease; colon tumor; colorectal tumor; cytostatic;

KW gastrointestinal disease; neoplasm; ss.

XX

OS Unidentified.

XX

PN WO2005054508-A2.

XX

PD 16-JUN-2005.  
XX  
PF 01-DEC-2004; 2004WO-IB004323.  
XX  
PR 01-DEC-2003; 2003US-0525987P.  
PR 01-DEC-2004; 2004US-00000688.  
XX  
PA (IPSO-) IPSOGEN.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (PAOL-) INST PAOLI CALMETTES IPC.  
XX  
PI Bertucci F, Houlgatte R, Birnbaum D, Debono S;  
XX  
DR WPI; 2005-435408/44.  
DR PC:NCBI; gi472990.  
XX  
PT Analyzing differential gene expression associated with histopathologic  
PT features of colorectal disease, involves detecting overexpression or  
PT underexpression of pool of polynucleotide sequences in colon tissues.  
XX  
PS Claim 1; SEQ ID NO 831; 154pp; English.  
XX  
CC The invention describes a method of analyzing (M1) differential gene  
CC expression associated with histopathologic features of colorectal  
CC disease, comprising detecting overexpression or underexpression of a pool  
CC of polynucleotide sequences in colon tissues, the pool selected in each  
CC of predefined polynucleotide sequence sets chosen from any one of 644  
CC sequence sets comprising combinations of SEQ ID No. 1-1596, fully defined  
CC in the specification. Also described are: a polynucleotide library (I)  
CC useful for the molecular characterization of a colon cancer, comprising  
CC or corresponding to a pool of polynucleotide sequences either  
CC overexpressed or underexpressed in colon tissue, the pool corresponding  
CC to all or part of the polynucleotide sequence chosen from PS1; and  
CC assigning (M2) a therapeutic regimen to patient with histopathological  
CC features of colorectal disease, e.g. colon cancer, comprising classifying  
CC the patient having a poor prognosis or a good prognosis on the basis of  
CC (M1), assigning the patient a therapeutic regimen, the therapeutic  
CC regiment comprising no adjuvant chemotherapy if the patient is lymph node  
CC negative and is classified as having a good prognosis or comprising  
CC chemotherapy if the patient has any other combination of lymph node  
CC status and expression profile. (M1) is useful for analyzing differential  
CC gene expression associated with histopathologic features of colorectal  
CC disease. (M1) is useful for analyzing differential gene expression  
CC associated with colon tumors, visceral metastases in colon cancer, lymph  
CC node metastases in colon cancer, MSI phenotype in colon cancer, location  
CC of primary colorectal carcinoma, in colon cancer, and survival and death  
CC of patient in colon cancer, where the analysis comprises detection of  
CC overexpression or underexpression of pool of polynucleotide sequences in  
CC colon tissue, the pool corresponding to specific combination of

CC polynucleotide sequences from PS1, as given in the specification. (M1) is  
CC useful for detecting, diagnosing, staging, classifying, monitoring or  
CC predicting conditions associated with colorectal cancer. (M1) is useful  
CC for prognosis or diagnosis or colon cancer or for monitoring the  
CC treatment of a patient with colon cancer, which involves implementing  
CC (M1) on nucleic acids from the patient. (M1) is useful for  
CC differentiating a normal cell from a cancer cell, which involves  
CC implementing (M1) on nucleic acids from the cells. (M1) is useful for  
CC selecting appropriate doses and/or schedule of chemotherapeutics and/or  
CC (bio)pharmaceuticals and/or target agents e.g. Irinotecan, 5-fluorouracil  
CC and methotrexate. This sequence represents a polynucleotide identified in  
CC the analysis of differential gene expression associated with  
CC histopathological features of colorectal disease. Note: The sequence data  
CC for this patent is not represented in the printed specification but is  
CC based on sequence information supplied by the European Patent Office.  
CC  
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed  
CC information from BOND.

XX

SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 99.9%; Score 3422.4; DB 4; Length 3424;  
Best Local Similarity 99.9%;  
Matches 3423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360

Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140

Db	1081	 CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	 CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	 CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	 GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	 GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	 AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	 TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	 CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTATAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	 CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	 TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	 AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860

Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGAAAAGCTCATTA ACTTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGAAAAGCTCATTA ACTTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCTGAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCTGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGA AAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGA AAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580



Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300

Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 6  
AED31618

ID	AED31618 standard; cDNA; 3424 BP.		
XX			
AC	AED31618;		
XX			
DT	15-DEC-2005 (first entry)		
XX			
DE	cDNA (SEQ ID No:2) encoding human phosphatidylinositol 3-kinase (PIK3CA).		
XX			
KW	cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;		
KW	chemotherapy; cytostatic; RNA interference; gene silencing;		
KW	antisense therapy; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	13. .3219	
FT		/*tag= a	
FT		/product= "PIK3CA"	
XX			
PN	WO2005091849-A2.		
XX			
PD	06-OCT-2005.		
XX			
PF	18-FEB-2005; 2005WO-US005193.		
XX			
PR	02-MAR-2004; 2004US-0548886P.		
XX			
PA	(UYJO ) UNIV JOHNS HOPKINS.		
XX			
PI	Samuels Y, Velculescu V, Kinzler KW, Vogelstein B;		
XX			
DR	WPI; 2005-713721/73.		
DR	P-PSDB; AED31619.		
XX			

PT     Assessing cancer in a human suspected of having cancer, by determining a  
PT     non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase  
PT     (PIK3CA) coding sequence in the body sample from a human.  
XX  
PS     Claim 1; SEQ ID NO 2; 107pp; English.  
XX  
CC     The invention relates to a method of assessing cancer in a body sample of  
CC     a human suspected of having cancer. The method comprises determining a  
CC     non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase  
CC     (PIK3CA) coding sequence in the body sample, and identifying the human as  
CC     likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA  
CC     coding sequence is determined in the body sample. Also described are: (1)  
CC     a method of inhibiting progression of a tumor in a human; (2) a method of  
CC     identifying candidate chemotherapeutic agents; (3) a method for  
CC     delivering an appropriate chemotherapeutic drug to a patient in need; and  
CC     (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,  
CC     the primers selected from forward primers, reverse primers, or sequencing  
CC     primers, where the forward primers are selected from sequences given as  
CC     SEQ ID NOs 6-165, the reverse primers are selected from sequences given  
CC     as SEQ ID NOs 166-325, and the sequencing primers are selected sequences  
CC     given as SEQ ID NOs 326-485 in the specification. The method of the  
CC     invention is useful for assessing cancer in a body sample of a human  
CC     suspected of having cancer, inhibiting progression of a tumor in a human,  
CC     identifying candidate chemotherapeutic agents, and delivering an  
CC     appropriate chemotherapeutic drug to a patient in need. This sequence  
CC     encodes human PIK3CA.  
XX  
SQ     Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match                    99.9%;    Score 3422.4;    DB 4;    Length 3424;  
Best Local Similarity    99.9%;  
Matches 3423;    Conservative    0;    Mismatches    1;    Indels    0;    Gaps    0;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240

Qy	241	GCAGAAAGGGAAGAATTTTTTGGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020

Db	961	 TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	 AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	 CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1141	 CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	 CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	 GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	 GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	 AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	 TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	 CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	 CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740

Db	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460

Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180

Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTC	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 7

AEG93388

ID	AEG93388	standard; cDNA; 3424 BP.
XX		
AC	AEG93388;	
XX		
DT	11-JUN-2007	(revised)
DT	01-JUN-2006	(first entry)
XX		
DE	Human tumor cell cDNA SEQ ID NO:884.	
XX		
KW	Gene expression; tumor; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2006036025-A1.	
XX		
PD	06-APR-2006.	
XX		
PF	30-SEP-2005; 2005WO-JP018574.	
XX		
PR	30-SEP-2004; 2004JP-00286259.	
PR	28-FEB-2005; 2005JP-00054475.	
PR	28-FEB-2005; 2005JP-00054866.	
XX		
PA	(EISA ) EISAI CO LTD.	
XX		
PI	Owa T, Yokoi A, Ozawa Y, Kawai T, Ushijima R;	



[illegible]CC  
CC  
XXXX  
SQ

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Query Match          99.9%;   Score 3422.4;   DB 4;   Length 3424;
Best Local Similarity 99.9%;
Matches 3423;   Conservative    0;   Mismatches    1;   Indels        0;   Gaps          0;
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Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840

Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620

Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCTGAATTATGTCTTCTGCAAAA	2340

Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060

Qy	3061	GATGACATTGCATACATTTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Db	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Db	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTT	3420
Qy	3421	AAAA 3424	
Db	3421	AAAA 3424	

RESULT 8  
AAQ51156  
ID AAQ51156 standard; cDNA; 3412 BP.  
XX  
AC AAQ51156;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-APR-1994 (first entry)  
XX  
DE Human p110 cDNA.  
XX  
KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist;  
KW cell proliferation; inhibition; prophylaxis; therapy; platelets;  
KW neutrophil activity; 3-phosphorylated phosphoinositides; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1. .3207

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Query Match          99.6%;   Score 3410.4;   DB 1;   Length 3412;
Best Local Similarity 99.9%;
Matches 3411;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy          13  ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC  72
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1  ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC  60

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Qy	73	CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAAATGCCTCCGTGAGGCT	132
Db	61	CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAAATGCCTCCGTGAGGCT	120
Qy	133	ACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA	192
Db	121	ACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA	180
Qy	193	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	252
Db	181	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	240
Qy	253	GAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTTAAAA	312
Db	241	GAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTTAAAA	300
Qy	313	GTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTTTGCT	372
Db	301	GTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTTTGCT	360
Qy	373	ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA	432
Db	361	ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA	420
Qy	433	AGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT	492
Db	421	AGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT	480
Qy	493	AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC	552
Db	481	AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC	540
Qy	553	ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA	612
Db	541	ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA	600
Qy	613	AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTA	672
Db	601	AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTA	660
Qy	673	ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA	732
Db	661	ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA	720
Qy	733	CTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC	792
Db	721	CTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC	780
Qy	793	TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG	852



Db	781	 TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG	840
Qy	853	AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC	912
Db	841	 AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC	900
Qy	913	TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA	972
Db	901	 TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA	960
Qy	973	GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAAATTCTTTGT	1032
Db	961	 GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAAATTCTTTGT	1020
Qy	1033	GCAACCTACGTGAATCTAAATATTTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC	1092
Db	1021	 GCAACCTACGTGAATCTAAATATTTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC	1080
Qy	1093	TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT	1152
Db	1081	 TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT	1140
Qy	1153	CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTCCTCGTGCTGCT	1212
Db	1141	 CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTCCTCGTGCTGCT	1200
Qy	1213	CGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT	1272
Db	1201	 CGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT	1260
Qy	1273	CCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA	1332
Db	1261	 CCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA	1320
Qy	1333	ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTGAACCCTATTGGT	1392
Db	1321	 ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTGAACCCTATTGGT	1380
Qy	1393	GTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC	1452
Db	1381	 GTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC	1440
Qy	1453	AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1512
Db	1441	 AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1500
Qy	1513	TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1572

Db	1501	TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1560
Qy	1573	AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC	1632
Db	1561	AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC	1620
Qy	1633	TCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1692
Db	1621	TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1680
Qy	1693	ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGATGAAGTA	1752
Db	1681	ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGATGAAGTA	1740
Qy	1753	GCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1812
Db	1741	GCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1800
Qy	1813	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAA	1872
Db	1801	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAA	1860
Qy	1873	AAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1932
Db	1861	AAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1920
Qy	1933	TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT	1992
Db	1921	TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT	1980
Qy	1993	CAAAGGATTGGGCACTTTTTCTTTTGGCATTAAATCTGAGATGCACAATAAAACAGTT	2052
Db	1981	CAAAGGATTGGGCACTTTTTCTTTTGGCATTAAATCTGAGATGCACAATAAAACAGTT	2040
Qy	2053	AGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG	2112
Db	2041	AGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG	2100
Qy	2113	CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACTGACATTCTCAA	2172
Db	2101	CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACTGACATTCTCAA	2160
Qy	2173	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTTGAGCAAATGAGG	2232
Db	2161	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTTGAGCAAATGAGG	2220
Qy	2233	CGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCATCA	2292
Db	2221	CGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCATCA	2280

Qy	2293	CTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGG	2352
Db	2281	CTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGG	2340
Qy	2353	TTGAATTGGGAGAACCCAGACATCATGTTCAGAGTTACTGTTTCAGAACAAATGAGATCATC	2412
Db	2341	TTGAATTGGGAGAACCCAGACATCATGTTCAGAGTTACTGTTTCAGAACAAATGAGATCATC	2400
Qy	2413	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG	2472
Db	2401	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG	2460
Qy	2473	GAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA	2532
Db	2461	GAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA	2520
Qy	2533	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCACACTATTATGCAAATT	2592
Db	2521	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCACACTATTATGCAAATT	2580
Qy	2593	CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG	2652
Db	2581	CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG	2640
Qy	2653	CTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2712
Db	2641	CTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2700
Qy	2713	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2772
Db	2701	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2760
Qy	2773	ATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2832
Db	2761	ATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820
Qy	2833	AAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTGACACAGGATTTC	2892
Db	2821	AAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTGACACAGGATTTC	2880
Qy	2893	TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT	2952
Db	2881	TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT	2940
Qy	2953	CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT	3012
Db	2941	CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT	3000

Qy	3013	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3072
Db	3001	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3060
Qy	3073	TACATTTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG	3132
Db	3061	TACATTTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG	3120
Qy	3133	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC	3192
Db	3121	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC	3180
Qy	3193	ACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3252
Db	3181	ACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3240
Qy	3253	TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3312
Db	3241	TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3300
Qy	3313	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA	3372
Db	3301	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA	3360
Qy	3373	TAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTCAAAA	3424
Db	3361	TAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTCAAAA	3412

RESULT 9  
AED31617  
ID AED31617 standard; cDNA; 3412 BP.  
XX  
AC AED31617;  
XX  
DT 15-DEC-2005 (first entry)  
XX  
DE cDNA (SEQ ID No:1) encoding human phosphatidylinositol 3-kinase (PIK3CA).  
XX  
KW cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;  
KW chemotherapy; cytostatic; RNA interference; gene silencing;  
KW antisense therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1. .3207  
FT /\*tag= a  
FT /product= "PIK3CA"

XX  
PN WO2005091849-A2.  
XX  
PD 06-OCT-2005.  
XX  
PF 18-FEB-2005; 2005WO-US005193.  
XX  
PR 02-MAR-2004; 2004US-0548886P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Samuels Y, Velculescu V, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2005-713721/73.  
DR P-PSDB; AED31619.  
XX  
PT Assessing cancer in a human suspected of having cancer, by determining a  
PT non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase  
PT (PIK3CA) coding sequence in the body sample from a human.  
XX  
PS Disclosure; SEQ ID NO 1; 107pp; English.  
XX  
CC The invention relates to a method of assessing cancer in a body sample of  
CC a human suspected of having cancer. The method comprises determining a  
CC non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase  
CC (PIK3CA) coding sequence in the body sample, and identifying the human as  
CC likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA  
CC coding sequence is determined in the body sample. Also described are: (1)  
CC a method of inhibiting progression of a tumor in a human; (2) a method of  
CC identifying candidate chemotherapeutic agents; (3) a method for  
CC delivering an appropriate chemotherapeutic drug to a patient in need; and  
CC (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,  
CC the primers selected from forward primers, reverse primers, or sequencing  
CC primers, where the forward primers are selected from sequences given as  
CC SEQ ID NOs 6-165, the reverse primers are selected from sequences given  
CC as SEQ ID NOs 166-325, and the sequencing primers are selected sequences  
CC given as SEQ ID NOs 326-485 in the specification. The method of the  
CC invention is useful for assessing cancer in a body sample of a human  
CC suspected of having cancer, inhibiting progression of a tumor in a human,  
CC identifying candidate chemotherapeutic agents, and delivering an  
CC appropriate chemotherapeutic drug to a patient in need. This sequence  
CC encodes human PIK3CA.  
XX  
SQ Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

Query Match 99.6%; Score 3410.4; DB 4; Length 3412;  
Best Local Similarity 99.9%;  
Matches 3411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	13	ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC	72
Db	1	ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC	60
Qy	73	CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT	132
Db	61	CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT	120
Qy	133	ACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA	192
Db	121	ACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA	180
Qy	193	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	252
Db	181	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	240
Qy	253	GAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTTAAAA	312
Db	241	GAATTTTTTGTATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTTAAAA	300
Qy	313	GTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTTTGCT	372
Db	301	GTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTTTGCT	360
Qy	373	ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA	432
Db	361	ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA	420
Qy	433	AGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT	492
Db	421	AGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT	480
Qy	493	AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC	552
Db	481	AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC	540
Qy	553	ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA	612
Db	541	ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA	600
Qy	613	AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTA	672
Db	601	AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTA	660
Qy	673	ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA	732
Db	661	ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA	720
Qy	733	CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC	792

Db	721	 CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC	780
Qy	793	TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG	852
Db	781	 TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG	840
Qy	853	AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC	912
Db	841	 AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC	900
Qy	913	TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA	972
Db	901	 TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA	960
Qy	973	GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAAATTCTTTGT	1032
Db	961	 GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAAATTCTTTGT	1020
Qy	1033	GCAACCTACGTGAATCTAAATATTTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC	1092
Db	1021	 GCAACCTACGTGAATCTAAATATTTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC	1080
Qy	1093	TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT	1152
Db	1081	 TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT	1140
Qy	1153	CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTTCCTCGTGCTGCT	1212
Db	1141	 CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTTCCTCGTGCTGCT	1200
Qy	1213	CGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT	1272
Db	1201	 CGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT	1260
Qy	1273	CCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA	1332
Db	1261	 CCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA	1320
Qy	1333	ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTGAACCCTATTGGT	1392
Db	1321	 ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTGAACCCTATTGGT	1380
Qy	1393	GTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC	1452
Db	1381	 GTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC	1440
Qy	1453	AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1512

Db	1441	AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1500
Qy	1513	TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1572
Db	1501	TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1560
Qy	1573	AATGAATTAAGGGAAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC	1632
Db	1561	AATGAATTAAGGGAAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC	1620
Qy	1633	TCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1692
Db	1621	TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1680
Qy	1693	ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCTAGAGATGAAGTA	1752
Db	1681	ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCTAGAGATGAAGTA	1740
Qy	1753	GCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1812
Db	1741	GCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1800
Qy	1813	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAA	1872
Db	1801	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAA	1860
Qy	1873	AAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1932
Db	1861	AAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1920
Qy	1933	TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT	1992
Db	1921	TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT	1980
Qy	1993	CAAAGGATTGGGCACTTTTTCTTTTGGCATTAAATCTGAGATGCACAATAAAACAGTT	2052
Db	1981	CAAAGGATTGGGCACTTTTTCTTTTGGCATTAAATCTGAGATGCACAATAAAACAGTT	2040
Qy	2053	AGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG	2112
Db	2041	AGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG	2100
Qy	2113	CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTTAAGTACATTCTCAA	2172
Db	2101	CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTTAAGTACATTCTCAA	2160
Qy	2173	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTTGAGCAAATGAGG	2232
Db	2161	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTTGAGCAAATGAGG	2220



Qy	2233	CGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCATCAA	2292
Db	2221	CGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCATCAA	2280
Qy	2293	CTAGGAAACCTCAGGCTTAAAGAGTGTCTGAATTATGTCTTCTGCAAAAAGGCCACTGTGG	2352
Db	2281	CTAGGAAACCTCAGGCTTAAAGAGTGTCTGAATTATGTCTTCTGCAAAAAGGCCACTGTGG	2340
Qy	2353	TTGAATTGGGAGAACCCAGACATCATGTCTCAGAGTTACTGTTTCAGAACAAATGAGATCATC	2412
Db	2341	TTGAATTGGGAGAACCCAGACATCATGTCTCAGAGTTACTGTTTCAGAACAAATGAGATCATC	2400
Qy	2413	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG	2472
Db	2401	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG	2460
Qy	2473	GAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA	2532
Db	2461	GAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA	2520
Qy	2533	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACTATTATGCAAATT	2592
Db	2521	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACTATTATGCAAATT	2580
Qy	2593	CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG	2652
Db	2581	CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG	2640
Qy	2653	CTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2712
Db	2641	CTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA	2700
Qy	2713	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2772
Db	2701	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2760
Qy	2773	ATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACACTTTTTGGATCAC	2832
Db	2761	ATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACACTTTTTGGATCAC	2820
Qy	2833	AAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTGACACAGGATTTT	2892
Db	2821	AAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTGACACAGGATTTT	2880
Qy	2893	TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT	2952
Db	2881	TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT	2940

Qy	2953	CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAAT	3012
Db	2941	CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAAT	3000
Qy	3013	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3072
Db	3001	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3060
Qy	3073	TACATTTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG	3132
Db	3061	TACATTTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG	3120
Qy	3133	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC	3192
Db	3121	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC	3180
Qy	3193	ACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3252
Db	3181	ACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3240
Qy	3253	TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3312
Db	3241	TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3300
Qy	3313	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA	3372
Db	3301	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA	3360
Qy	3373	TAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTCAAAA	3424
Db	3361	TAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATTTCAAAA	3412

RESULT 10  
ADU05935  
ID ADU05935 standard; DNA; 3423 BP.  
XX  
AC ADU05935;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Novel bronchial cancer-associated human gene SeqID157.  
XX  
KW bronchial cancer; cytostatic; tumour-associated protein;  
KW cancer detection; metastasis; tumour; gene; ds; human.  
XX  
OS Homo sapiens.  
XX  
PN DE10316701-A1.

09-APR-2003; 2003DE-01016701.

09-APR-2003; 2003DE-01016701.

(HINZ/) HINZMANN B.

(HERM/) HERMANN K.

(CAST/) HEIDEN CASTANOS-VELEZ E.

Mennerich D, Bruemmendorf T, Heiden E, Hermann K, Kinnemann H;  
Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;

WPI; 2004-786403/78.

P-PSDB; ADU06422.

New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.

Claim 1; SEQ ID NO 157; 1381pp; German.

This invention relates to a novel isolated nucleic acid associated with bronchial cancer comprising 489 defined sequences given in the specification. The invention may be useful for the production of compounds with a cytostatic activity through the inhibition of expression or activity of tumour-associated proteins. The novel DNA sequences and the proteins/peptides encoded by them are used for detecting bronchial cancer or determining the risk of developing it and to screen for specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or diagnosing bronchial cancer. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment (of tumours that have been stabilised or are no longer detectable). Detecting abnormal expression of the DNA sequences provides early diagnosis of bronchial cancers. The present sequence is that of a novel bronchial cancer-associated human gene sequence of the invention.

Sequence 3423 BP; 1134 A; 618 C; 709 G; 962 T; 0 U; 0 Other;

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Query Match      99.6%;   Score 3410.4;   DB 3;   Length 3423;
Best Local Similarity 99.9%;
Matches 3422;   Conservative    0;   Mismatches    1;   Indels    1;   Gaps    1;
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Qy      1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy     61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120

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Db	61	 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	241	 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	 CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	 ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	 CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAGTGGTGATTTGGGTA	600
Db	541	 CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAGTGGTGATTTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	 ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	 CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	721	 GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840

Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560

Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280

Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060

Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTG-TAATAACTCTCAGCAGGCAAAGACCGATTGCA	3299
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3360
Db	3300	TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT	3359
Qy	3361	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC	3420
Db	3360	ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC	3419
Qy	3421	AAAA 3424	
Db	3420	AAAA 3423	

RESULT 11

ARC02473

ID	ARC02473	standard; DNA; 3426 BP.
XX		
AC	ARC02473;	
XX		
DT	10-JUL-2008	(first entry)
XX		
DE	DNA fragments of a human Tox gene,	46524.
XX		
KW	DNA microarray; gene expression; drug screening; ds; Tox.	
XX		
OS	Homo sapiens.	
XX		
PN	US2007072175-A1.	
XX		
PD	29-MAR-2007.	



XX  
PF 15-MAY-2006; 2006US-00433832.  
XX  
PR 13-MAY-2005; 2005US-0680473P.  
PR 13-MAY-2005; 2005US-0680544P.  
XX  
PA (BIOJ ) BIOGEN IDEC MA INC.  
XX  
PI Cooper MT, Kinch D, Rosenberg M, Subramaniam SS, Szak ST, Li H;  
PI Bandaru R, Derbel M;  
XX  
DR WPI; 2007-432796/41.  
XX  
PT New nucleotide array comprises polynucleotide probes complementary to, or  
PT fragments of, Cynomolgus monkey genes, useful for detecting changes in  
PT gene expression upon administration of a therapeutic agent.  
XX  
PS Claim 18; SEQ ID NO 46524; 33pp; English.  
XX  
CC The new invention relates to a nucleotide array for detecting changes in  
CC gene expression upon administration of a therapeutic agent. The  
CC microarray has polynucleotide probes complementary to, or fragments of,  
CC Cynomolgus monkey genes, where each polynucleotide probe is immobilized  
CC to a discrete and known spot on a solid support. The polynucleotide  
CC probes are complementary to, or fragments of, any portion of an ortholog  
CC of a human gene, preferably a Tox gene. The probes are any of SEQ ID NO.  
CC 8882-9186. The probes are also complementary to, or fragments of, any  
CC portion of any of SEQ ID NO. 1-8881 or 9187-18598. The nucleotide array  
CC has at least one probe complementary to, or a fragment of, any portion of  
CC any human gene, where the probe from a human gene is any of SEQ ID NO.  
CC 43226-48714, or is complementary to, or a fragment of, any portion of any  
CC of SEQ ID NO. 43450-48714. The array has at least one probe complementary  
CC to, or a fragment of, any portion of any Rhesus monkey gene, where the  
CC probe from a Rhesus monkey gene is any of SEQ ID NO. 35841-36074, or is  
CC complementary to, or a fragment of, any portion of any of SEQ ID NO.  
CC 18599-35840 or 36075-43225. It also has at least one probe complementary  
CC to, or a fragment of, any portion of a Rhesus monkey gene and at least  
CC one probe complementary to, or a fragment of, any portion of any human  
CC gene. The nucleotide array is useful for detecting changes in gene  
CC expression upon administration of a therapeutic agent. It can be used for  
CC characterizing the actions, targets, and toxicities of therapeutic agents  
CC in primates, e.g. a human, a Cynomolgus monkey, or a Rhesus monkey. This  
CC sequence is a DNA fragment of a human Tox gene.  
XX  
SQ Sequence 3426 BP; 1138 A; 623 C; 703 G; 962 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 6; Length 3426;  
Best Local Similarity 98.8%;  
Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	1	AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Qy	61	CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAATAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	181	CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA	240
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTTCAA	300
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCCTTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAAGAAGCTGTGGATCTTAGGGACCTC	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA	540
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAAAGTGGTGATTTGGGTA	600
Db	541	TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAAAGTGGTGATCTGGGTA	600
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA	660
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT	720

Qy	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	721	GAACAATAAACTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	841	ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCCTCAGAATA	1020
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1021	AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGAAGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500

Db	1441	 TTTGA	CTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560	
Db	1501	 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560	
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620	
Db	1561	 CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620	
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680	
Db	1621	 CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680	
Qy	1681	TATTGTGTA	ACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1681	 TATTGTGTA	ACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800	
Db	1741	 AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800	
Qy	1801	CAGGCTATGGA	ACTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Db	1801	 CAGGCTATGGA	ACTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGA	AAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	1861	 CGGTGCTTGGA	AAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Qy	1921	CAGGTCCTAAA	ATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	1921	 CAGGTCCTAAA	ATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTA	ATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAATCTGAGATGCAC	2040
Db	1981	 GCATTGACTA	ATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGT	TAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	 AATAAAACAGT	TAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTTGA	AGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTA	2160
Db	2101	 ATGTATTTGA	AGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTA	2160
Qy	2161	GACATTCTCAA	ACAGGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220

Db	2161	GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCTGAATTATGTCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCTGAATTATGTCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940

Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA	3239
Db	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA	3240
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3241	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3300
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3301	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA	3360
Qy	3359	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3418
Db	3361	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3420
Qy	3419	TCAAAA 3424	
Db	3421	TCAAAA 3426	

RESULT 12  
AEK54940  
ID AEK54940 standard; DNA; 3724 BP.  
XX  
AC AEK54940;  
XX  
DT 11-JUN-2007 (revised)  
DT 16-NOV-2006 (first entry)  
XX  
DE Human PIK3CA DNA, SEQ ID NO:7.  
XX

KW phosphoinositide-3-kinase, catalytic, alpha; PIK3CA; genetic marker;  
KW screening; adenocarcinoma; neoplasm; cytostatic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2006094149-A2.  
XX  
PD 08-SEP-2006.  
XX  
PF 01-MAR-2006; 2006WO-US007493.  
XX  
PR 01-MAR-2005; 2005US-0657841P.  
XX  
PA (EXAC-) EXACT SCI CORP.  
XX  
PI Shuber AP;  
XX  
DR WPI; 2006-680485/70.  
DR REFSEQ; NM\_006218.  
DR PC:NCBI; gi54792081.  
DR PC\_ENCPRO:NCBI; gi54792082.  
XX  
PT Screening for adenoma in a subject, comprises testing a sample for the  
PT presence of each of a panel of genetic markers, where the panel is more  
PT than 60% informative for adenoma.  
XX  
PS Disclosure; SEQ ID NO 7; 79pp; English.  
XX  
CC The invention relates to a method for screening a subject for the  
CC presence of adenoma. The method comprises interrogating a sample from the  
CC subject for each of a panel of genetic markers, where the panel is more  
CC than 60% informative for adenoma, and where the presence of one or more  
CC of the markers is indicative of adenoma. Also described are: (1) a method  
CC of detecting indicia of adenoma, by assaying a sample from a subject for  
CC the presence of one or more genetic abnormalities from a group of genetic  
CC abnormalities that is more than 60% informative for adenoma; (2) a method  
CC of detecting adenoma in a subject, by performing an assay on a sample  
CC from the subject that is more than 60% informative for adenoma; and (3) a  
CC kit comprising a group of oligonucleotides, where each oligonucleotide is  
CC adapted for interrogating a genetic locus for the presence of a marker  
CC from a panel that is at least 60% informative for adenoma. The methods  
CC and kit of the invention are useful for screening for adenoma in a  
CC subject. The adenoma is especially a colonic and/or invasive adenoma. The  
CC methods can detect adenoma at an early stage with a high level of  
CC confidence, increasing the chances of successful treatment. This sequence  
CC represents a human DNA sequence that can be used as a genetic marker in  
CC the method of the invention.  
CC  
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed

CC information from BOND.  
XX  
SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 4; Length 3724;  
Best Local Similarity 98.8%;  
Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	205
Qy	61	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	206	CCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	265
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	266	CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	325
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	326	CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA	385
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	386	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTTCAA	445
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCCTTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	506	ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAAGAAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	626	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA	685
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	686	TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA	745
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660



Db	746	 ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA	805
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	 CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT	865
Qy	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGGA	780
Db	866	 GAACAACATAAACTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAGTGTGTGGA	925
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926	 TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	985
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	986	 ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	1046	 CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	1106	 TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCCTCAGAATA	1165
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1166	 AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1226	 CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1285
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1286	 CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1345
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1346	 CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1406	 GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1465
Qy	1321	GATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380

Db	1466	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1525
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1526	AACCCTATTGGTGTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1765
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1766	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	1860
Db	1946	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTTCGAGGTTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	2006	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	2065
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	2066	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2186	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2245

Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTA ACTTAACT	2160
Db	2246	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTA ACTTAACT	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCGACCAGATTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCGAATTATGTCTTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2545
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2725
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2846	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAAC TGTTTCATATAGATTTTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAAGACGATGGACAAC TGTTTCATATAGATTTTGGACAC	2965

Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2966	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	3025
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3146	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3205
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3206	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3265
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAAATGAA	3239
Db	3326	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT	3418
Db	3506	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

RESULT 13  
AER29796  
ID AER29796 standard; DNA; 3724 BP.  
XX

AC AER29796;  
XX  
DT 11-JUN-2007 (revised)  
DT 22-MAR-2007 (first entry)  
XX  
DE Breast cancer-associated gene SEQ ID NO:97.  
XX  
KW diagnosis; breast tumor; biochip; tumor marker; genetic marker;  
KW biomarker; DNA detection; RNA detection; ds; PIK3CA.  
XX  
OS Homo sapiens.  
XX  
PN WO2007006911-A2.  
XX  
PD 18-JAN-2007.  
XX  
PF 05-JUL-2006; 2006WO-FR001593.  
XX  
PR 07-JUL-2005; 2005FR-00052087.  
XX  
PA (INMR ) BIOMERIEUX SA.  
XX  
PI Krause A, Leissner P, Mougin B, Paye M;  
XX  
DR WPI; 2007-138577/14.  
DR PC:NCBI; gi54792081.  
DR PC\_ENCPRO:NCBI; gi54792082.  
XX  
PT In vitro diagnosis of breast cancer comprises extracting biological  
PT material of biological sample, contacting biological material with  
PT specific reagents of target genes and determining target gene expression.  
XX  
PS Example 2; SEQ ID NO 97; 305pp; French.  
XX  
CC The invention describes a method for in vitro diagnosis of breast cancer  
CC in a patient susceptible to be affected by breast cancer, comprising:  
CC extracting nucleic acid from a biological sample taken from the patient;  
CC contacting the nucleic acid with at least 8 hybridization probes for  
CC detection of target genes chosen from SEQ ID Nos. 1 to 8 or 10 probes for  
CC detection of target genes chosen from SEQ ID Nos. 1, 2, 4, 6, 13, 14, 26,  
CC 69, 81 and 105; and determining the expression of the target genes. The  
CC invention also includes: a support, such as a biochip, comprising at  
CC least 8 or 10 hybridization probes mentioned above; and a diagnosis kit  
CC for breast cancer comprising the support. The method, biochip and kit are  
CC useful for the in vitro diagnosis of breast cancer. This sequence is a  
CC breast cancer-associated gene.  
CC  
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed  
CC information from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 5; Length 3724;

Best Local Similarity 98.8%;

Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	205
Qy	61	CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGAAGTTTAGAATGC	120
Db	206	CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGAAGTTTAGAATGC	265
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	266	CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	325
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	326	CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA	385
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	386	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA	445
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCCTTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	506	ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAGAAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	626	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA	685
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	686	TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA	745
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660

Db	746	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA	805
Qy	661	CCAGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT	865
Qy	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	866	GAACAATAAACTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA	925
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	985
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	986	ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	1046	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCCTCAGAATA	1165
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1166	AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1285
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1200
Db	1286	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT	1345
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1346	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1406	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1465
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1466	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1525

Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1526	AACCCTATTGGTGTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1765
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1766	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACCTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1946	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	2006	CGGTGCTTGGA AAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	2065
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	2066	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2186	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2245



Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTTAAC	2160
Db	2246	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTTAAC	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCGACCAGATTTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCTGAATTATGTCTTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCTGAATTATGTCTTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2545
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2725
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2846	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2965
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880

Db	2966	 TTTTTGGATCACAAGAAGAAAAAATTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	3025
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	3026	 ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	3086	 TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3146	 CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3205
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3206	 GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3265
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	 GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA	3239
Db	3326	 TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	 AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	 ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3418
Db	3506	 CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424 	
Db	3566	TCAAAA 3571	

RESULT 14  
ARV60468  
ID ARV60468 standard; cDNA; 3724 BP.  
XX  
AC ARV60468;

XX  
DT 24-JUL-2008 (first entry)  
XX  
DE Human PIK3CA polynucleotide, SEQ ID 30.  
XX  
KW mutation; dna microarray; prognosis; diagnostic test; therapeutic;  
KW non-small-cell lung cancer; tumor; cytostatic; ss; gene;  
KW phosphoinositide-3-kinase, catalytic, alpha polypeptide; PIK3CA.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 158. .3364  
FT /\*tag= a  
FT /product  
XX  
PN WO2008061213-A2.  
XX  
PD 22-MAY-2008.  
XX  
PF 15-NOV-2007; 2007WO-US084888.  
XX  
PR 16-NOV-2006; 2006US-0866103P.  
PR 10-JUL-2007; 2007US-0948818P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Seshagiri S, Peters B, Kan Z;  
XX  
DR WPI; 2008-G25985/39.  
DR P-PSDB; ARV60505.  
DR PC:NCBI; gi54792081.  
DR PC\_ENCPRO:NCBI; gi54792082.  
XX  
PT New isolated polynucleotide comprises PRO polynucleotide or fragment  
PT comprising a nucleotide variation, useful for detecting nucleotide  
PT variations for diagnosing and treating tumors.  
XX  
PS Claim 2; SEQ ID NO 30; 55pp; English.  
XX  
CC The present invention relates to a novel isolated polynucleotide  
CC comprising a PRO polynucleotide or its fragment. The PRO polynucleotide  
CC or its fragment comprises a nucleotide variation at a nucleotide position  
CC given in the specification. A nucleotide variation refers to a change in  
CC a nucleotide sequence (e.g., an insertion, deletion, inversion, or  
CC substitution of one or more nucleotides, such as a single nucleotide  
CC polymorphism (SNP)) relative to a reference sequence (e.g., a wild type  
CC sequence). A nucleotide variation may be a somatic mutation or a germline  
CC polymorphism. The present invention provides: (i) an allele-specific

oligonucleotide that hybridizes to a region of a PRO polynucleotide comprising a nucleotide variation at a nucleotide position, or its complement; (ii) a kit comprising the oligonucleotide and an enzyme; (iii) a microarray comprising the oligonucleotide; (iv) a method for detecting the absence or presence of the variation at a nucleotide position; (v) a method for amplifying a nucleic acid comprising the nucleotide variation; (vi) a method for determining the genotype of a biological sample (e.g. non-small cell lung carcinoma sample) from a mammal; (vii) a method for classifying a tumor in the mammal; and (viii) a method for predicting whether a tumor (e.g. non-small cell lung carcinoma) will respond to a therapeutic agent that targets a PRO or a PRO polynucleotide, comprises determining whether the tumor comprises a variation in a PRO or PRO polynucleotide, where the presence of a variation indicates that the tumor will respond to the therapeutic agent. The method of detecting the absence or presence of the nucleotide variation comprises: (a) contacting the suspected nucleic acid with the allele-specific oligonucleotide that is specific for the nucleotide variation, under conditions suitable for hybridization of the oligonucleotide to the nucleic acid; and (b) detecting the absence or presence of allele-specific hybridization. The method of amplifying the nucleic acid comprising the nucleotide variation comprises: (a) contacting the nucleic acid with a primer that hybridizes to the nucleic acid at 3' of the nucleotide variation; and (b) extending the primer to generate an amplification product comprising the nucleotide variation. The isolated polynucleotide is used for detecting nucleotide variations. The methods are used for diagnosing and treating tumors. The present sequence is a human PRO polynucleotide sequence used in the invention.

Revised record issued on 18-JUN-2008 : Enhanced with precomputed information from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 7; Length 3724;  
Best Local Similarity 98.8%;  
Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	205
Qy	61	CCCCAAGAATCCTAGTGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	206	CCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	265
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	266	CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	325

Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	326	CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA	385
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTTCAA	300
Db	386	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTTCAA	445
Qy	301	CCATTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCCTTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	506	ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAAGAAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	626	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA	685
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	686	TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA	745
Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	746	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA	805
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT	865
Qy	721	GAACAATTAAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	866	GAACAACATAAACTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA	925
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	985
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	986	ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960

Db	1046	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACCTCAGAATA	1165
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1166	AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1285
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1286	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1345
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1346	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1406	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1465
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380
Db	1466	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1525
Qy	1381	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1526	AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1765
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680

Db	1766	CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTA ACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGT TAAATGGAATTCT	1740
Db	1826	TATTGTGTA ACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGT TAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCC CAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCC CAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGA ACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1946	CAGGCTATGGA ACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	2006	CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	2065
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	2066	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGGCAC TTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATTGGGCAC TTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2186	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2245
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTA ACTTAACT	2160
Db	2246	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTA ACTTAACT	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCGACCAGATTT CATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCGACCAGATTT CATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCGAATTATGTCTTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2545

Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGGAAAATATCTGGCAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2725
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2846	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAAC TGTTTCATATAGATTTTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAAGACGATGGACAAC TGTTTCATATAGATTTTGGACAC	2965
Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2966	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	3025
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3146	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3205
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3206	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3265



Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAAATGAA	3239
Db	3326	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT	3418
Db	3506	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

RESULT 15

ARW65283

ID ARW65283 standard; cDNA; 3724 BP.

XX

AC ARW65283;

XX

DT 07-AUG-2008 (first entry)

XX

DE Human PIK3CA cDNA, SEQ ID 53.

XX

KW tumor marker; prognosis; diagnostic test; cancer; ss; gene; PIK3CA.

XX

OS Homo sapiens.

XX

PN WO2008070325-A2.

XX

PD 12-JUN-2008.

XX

PF 24-OCT-2007; 2007WO-US082397.

XX

PR 26-OCT-2006; 2006US-0863106P.

PR 14-MAY-2007; 2007US-0917814P.

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PA (GETH ) GENENTECH INC.

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DR WPI; 2008-G69314/42.

DR P-PSDB; ARW65361.

DR PC:NCBI; gi54792081.

DR PC\_ENCPRO:NCBI; gi54792082.

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PT New polynucleotide, useful for determining the genotype of a sample from  
PT a mammal, for classifying a tumor in a mammal or for predicting whether a  
PT tumor will respond to a therapeutic agent that targets a PRO polypeptide  
PT or polynucleotide.

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PS Claim 2; SEQ ID NO 53; 98pp; English.

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CC The present invention relates to novel isolated polynucleotides. An  
CC isolated polynucleotide comprises: (a) a PRO polynucleotide or its  
CC fragment that is at least about 10 nucleotides in length or that  
CC comprises a nucleotide variation at a nucleotide position given in the  
CC specification, or (b) its complement. These variations provide biomarkers  
CC for cancer and/or predisposition to tumorigenesis or tumor promotion. The  
CC present invention provides: (1) a kit comprising the oligonucleotide and  
CC at least one enzyme; (2) a microarray comprising the oligonucleotide; (3)  
CC a method for detecting the absence or presence of a nucleotide variation  
CC at a nucleotide position given in the specification, which comprises  
CC contacting the nucleic acid suspected of comprising the nucleotide  
CC variation with an allele-specific oligonucleotide that is specific for  
CC the nucleotide variation and detecting the absence or presence of allele-  
CC specific hybridization; (4) a method for amplifying a nucleic acid  
CC comprising a nucleotide variation at a nucleotide position given in the  
CC specification; (5) a method for determining the genotype of a tumor  
CC sample from a mammal; (6) a method for classifying a tumor in a mammal by  
CC detecting the presence of a variation in a PRO or PRO polynucleotide in a  
CC biological sample derived from the mammal; and (7) a method for  
CC predicting whether a tumor will respond to a therapeutic agent that  
CC targets a PRO or a PRO polynucleotide by determining whether the tumor  
CC comprises a variation in a PRO or PRO polynucleotide, where the presence  
CC of a variation indicates that the tumor will respond to the therapeutic  
CC agent. The method of amplifying a nucleic acid comprising a nucleotide  
CC variation comprises: (a) contacting the nucleic acid with a primer that  
CC hybridizes to the nucleic acid at a sequence 3' of the nucleotide  
CC variation, and (b) extending the primer to generate an amplification  
CC product comprising the nucleotide variation. The variations disclosed in  
CC the invention are useful in methods and compositions related to cancer  
CC diagnosis and therapy. The present sequence is an isolated polynucleotide  
CC of the invention.

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CC Revised record issued on 09-JUL-2008 : Enhanced with precomputed infor

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CC    Revised record issued on 09-JUL-2008 : mation from BOND.  
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SQ    Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;  
  
Query Match                    97.5%;    Score 3338;    DB 7;    Length 3724;  
Best Local Similarity    98.8%;  
Matches 3384;    Conservative    0;    Mismatches    40;    Indels        2;    Gaps        2;

Qy	1	AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	205
Qy	61	CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	206	CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	265
Qy	121	CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	180
Db	266	CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC	325
Qy	181	CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA	240
Db	326	CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA	385
Qy	241	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA	300
Db	386	GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA	445
Qy	301	CCATTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCCTTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA	420
Db	506	ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAGAAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG	540
Db	626	AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCAAATGTAGAATCTTCACCAGAA	685
Qy	541	CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA	600
Db	686	TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA	745

Qy	601	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	746	ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA	805
Qy	661	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT	865
Qy	721	GAACAATTAAACTCTGTGTTTTAGAAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA	780
Db	866	GAACAATAAACTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA	925
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	985
Qy	841	ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA	900
Db	986	ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960
Db	1046	CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACTCAGAATA	1165
Qy	1021	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT	1080
Db	1166	AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA	1285
Qy	1141	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1286	CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1345
Qy	1201	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1260
Db	1346	CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGGTGCTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1320
Db	1406	GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA	1465
Qy	1321	GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1380

Db	1466	 GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG	1525
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1526	 AACCCTATTGGTGTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	 TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1620
Db	1706	 CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA	1765
Qy	1621	CGAGATCCTCTCTCTAAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1680
Db	1766	 CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1740
Db	1826	 TATTGTGTAACATATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1886	 AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	1860
Db	1946	 CAGGCTATGGAACCTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGA AAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	1920
Db	2006	 CGGTGCTTGGA AAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA	2065
Qy	1921	CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	1980
Db	2066	 CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	2126	 GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCATTTAAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2100

Db	2186	AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG	2245
Qy	2101	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTTAAC	2160
Db	2246	ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTTAAC	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCGACCAGATTTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCGACCAGATTTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCTGAATTATGTCTTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCTGAATTATGTCTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2545
Qy	2401	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT	2725
Qy	2581	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2760
Db	2846	TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATTTTGGACAC	2965

Qy	2821	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	2880
Db	2966	TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG	3025
Qy	2881	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3060
Db	3146	CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT	3205
Qy	3061	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3206	GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG	3265
Qy	3121	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA	3239
Db	3326	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3418
Db	3506	CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

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